

# Package ‘babelgene’

May 7, 2026

**Type** Package

**Title** Gene Orthologs for Model Organisms in a Tidy Data Format

**Version** 22.9

**Description** Genomic analysis of model organisms frequently requires the use of databases based on human data or making comparisons to patient-derived resources. This requires harmonization of gene names into the same gene space. The 'babelgene' R package converts between human and non-human gene orthologs/homologs. The package integrates orthology assertion predictions sourced from multiple databases as compiled by the HGNC Comparison of Orthology Predictions (HCOP) (Wright et al. 2005 <[doi:10.1007/s00335-005-0103-2](https://doi.org/10.1007/s00335-005-0103-2)>, Eyre et al. 2007 <[doi:10.1093/bib/bbl030](https://doi.org/10.1093/bib/bbl030)>, Seal et al. 2011 <[doi:10.1093/nar/gkq892](https://doi.org/10.1093/nar/gkq892)>).

**License** MIT + file LICENSE

**URL** <https://igordot.github.io/babelgene/>

**BugReports** <https://github.com/igordot/babelgene/issues>

**Depends** R (>= 3.4)

**Imports** dplyr, methods, rlang

**Suggests** covr, knitr, rmarkdown, testthat (>= 3.0.0)

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**Encoding** UTF-8

**RoxygenNote** 7.2.1

**NeedsCompilation** no

**Author** Igor Dolgalev [aut, cre] (ORCID:  
<<https://orcid.org/0000-0003-4451-126X>>)

**Maintainer** Igor Dolgalev <[igor.dolgalev@nyumc.org](mailto:igor.dolgalev@nyumc.org)>

**Repository** CRAN

**Date/Publication** 2022-09-29 09:40:17 UTC

## Contents

orthologs . . . . .	2
species . . . . .	3

<b>Index</b>	<b>4</b>
--------------	----------

orthologs	<i>Retrieve gene orthologs/homologs</i>
-----------	---

### Description

Retrieve gene orthologs/homologs for a set of genes. Converts between human and non-human analogs.

### Usage

```
orthologs(genes, species, human = TRUE, min_support = 3, top = TRUE)
```

### Arguments

genes	A vector of gene symbols or Entrez/Ensembl IDs.
species	Species name, such as <i>Mus musculus</i> or mouse (see <code>species()</code> for options).
human	A logical scalar indicating if the input genes are human. If TRUE, the input genes are human. If FALSE, the input genes correspond to the non-human species and the output will be the human equivalents.
min_support	Minimum number of supporting source databases. Gene pairs available in this package are supported by 2 to 12 databases (the maximum varies depending on the species).
top	For each gene, output only the match with the highest support level if there are multiple hits.

### Value

A data frame of gene pairs (human and given species).

### References

Wright MW, Eyre TA, Lush MJ, Povey S, Bruford EA. HCOP: the HGNC comparison of orthology predictions search tool. *Mamm Genome*. 2005 Nov;16(11):827-8. doi:10.1007/s0033500501032

Eyre TA, Wright MW, Lush MJ, Bruford EA. HCOP: a searchable database of human orthology predictions. *Brief Bioinform*. 2007 Jan;8(1):2-5. doi:10.1093/bib/bbl030

Seal RL, Gordon SM, Lush MJ, Wright MW, Bruford EA. genenames.org: the HGNC resources in 2011. *Nucleic Acids Res*. 2011 Jan;39:D514-9. doi:10.1093/nar/gkq892

### Examples

```
orthologs(genes = "TP53", species = "mouse", human = TRUE)
orthologs(genes = c("Ptprc", "Cd34"), species = "mouse", human = FALSE)
```

---

species	<i>Retrieve the available species</i>
---------	---------------------------------------

---

**Description**

List the species with available human orthologs.

**Usage**

```
species(species = NULL)
```

**Arguments**

species	Species name, such as <i>Mus musculus</i> or mouse. If specified, will return results for the given species only.
---------	---

**Value**

A data frame of the available species.

**Examples**

```
species()  
species("Mus musculus")  
species("mouse")  
species("rat")
```

# Index

orthologs, 2

species, 3

species(), 2